

FIGURE 1

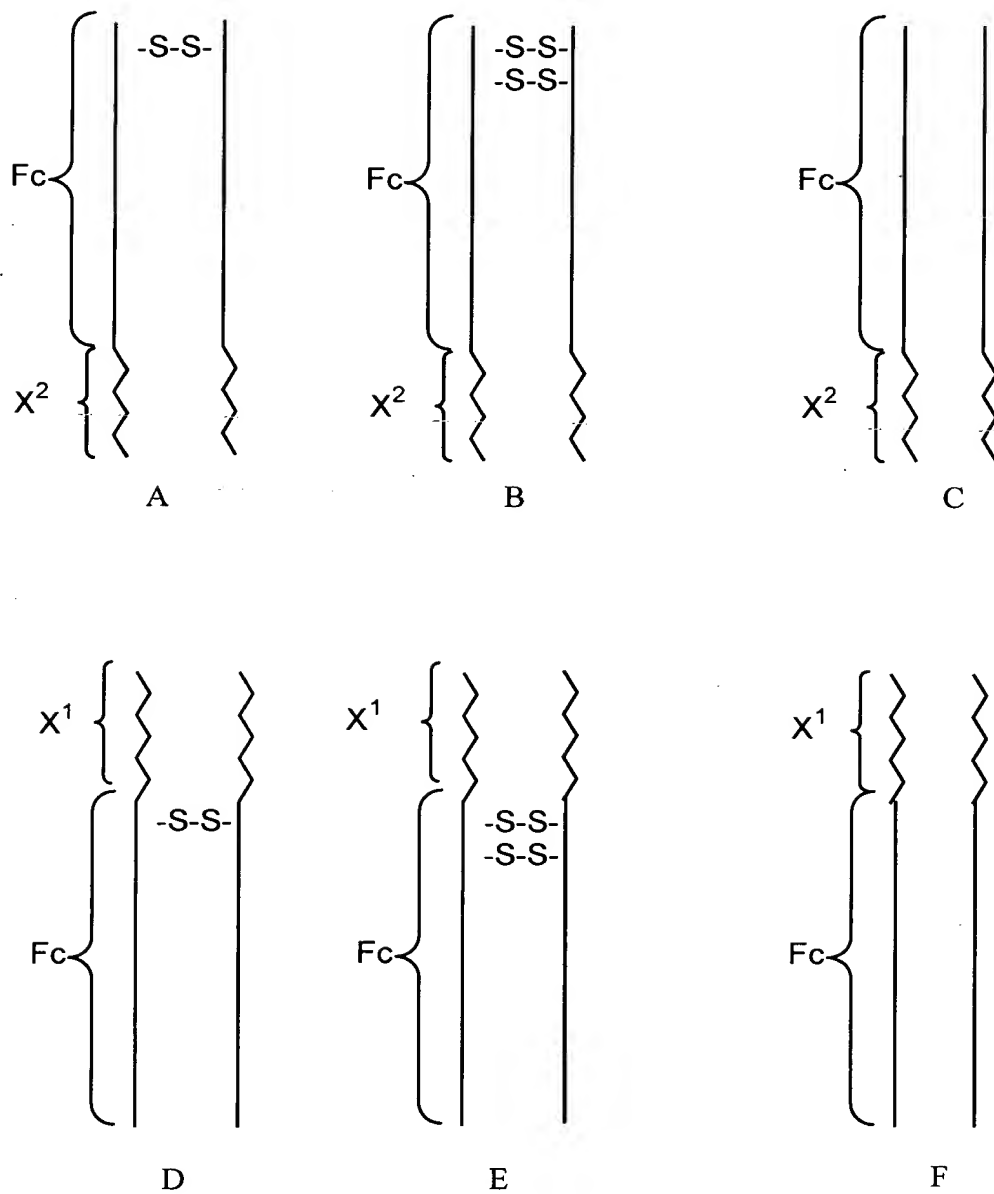


FIGURE 2

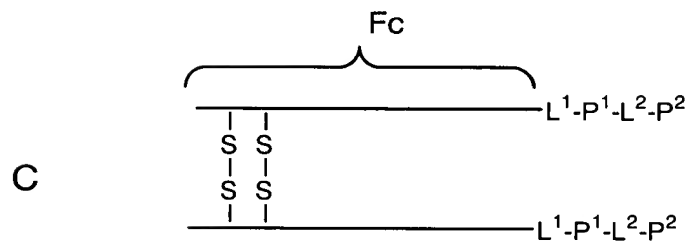
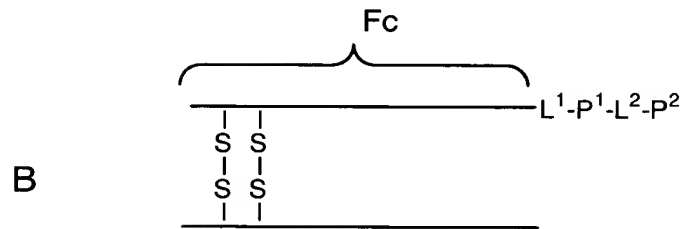
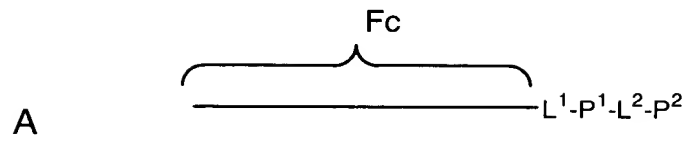


FIGURE 3A

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ATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCGTCA
1  -----+-----+-----+-----+-----+-----+-----+ 60
TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGT

a      M D K T H T C P P C P A P E L L G G P S -

GTCTTCCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTC
61  -----+-----+-----+-----+-----+-----+-----+ 120
CAGAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG

a      V F L F P P K P K D T L M I S R T P E V -

ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
121 -----+-----+-----+-----+-----+-----+-----+ 180
TGTACGCACCACCACCTGCACCTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC

a      T C V V V D V S H E D P E V K F N W Y V -

GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGC
181 -----+-----+-----+-----+-----+-----+-----+ 240
CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC

a      D G V E V H N A K T K P R E E Q Y N S T -

TACCGTGTGGTCAGCGTCCTCACCCTGCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
241 -----+-----+-----+-----+-----+-----+-----+ 300
ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATG

a      Y R V V S V L T V L H Q D W L N G K E Y -

AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
301 -----+-----+-----+-----+-----+-----+-----+ 360
TTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG

a      K C K V S N K A L P A P I E K T I S K A -

AAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACC
361 -----+-----+-----+-----+-----+-----+-----+ 420
TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGG

a      K G Q P R E P Q V Y T L P P S R D E L T -

AAGAACCAGGTGACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
421 -----+-----+-----+-----+-----+-----+-----+ 480
TTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC

a      K N Q V S L T C L V K G F Y P S D I A V -

GAGTGGGAGAGCAATGGGCAGCCGAGAACAATAAGACCACGCCCTCCCGTGTCTGGAC
481 -----+-----+-----+-----+-----+-----+-----+ 540
CTCACCTCTCGTTACCCGTCGGCCTCTTGTGTGATGTTCTGGTGCGGAGGGCAGCAGCTG

a      E W E S N G Q P E N N Y K T T P P V L D -

TCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
541 -----+-----+-----+-----+-----+-----+-----+ 600
AGGCTGCCGAGGAAGAAGGAGATGTCTGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTC

a      S D G S F F L Y S K L T V D K S R W Q Q -

GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
601 -----+-----+-----+-----+-----+-----+-----+ 660
CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGTGATGTGCGTCTTC

a      G N V F S C S V M H E A L H N H Y T Q K -

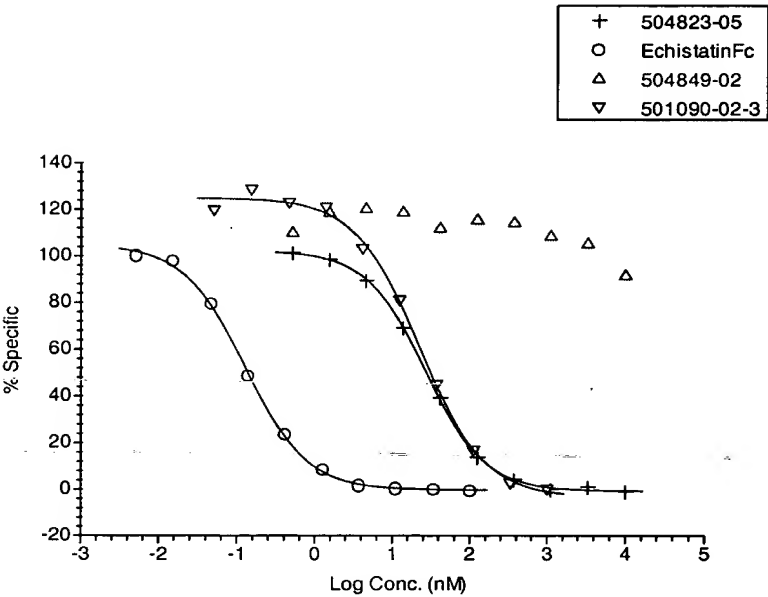
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FIGURE 3B

661 AGCCTCTCCCTGTCTCCGGGTAAA 684
-----+-----+-----
TCGGAGAGGGACAGAGGCCCATTT
a S L S L S P G K

FIGS. 4A and 4B

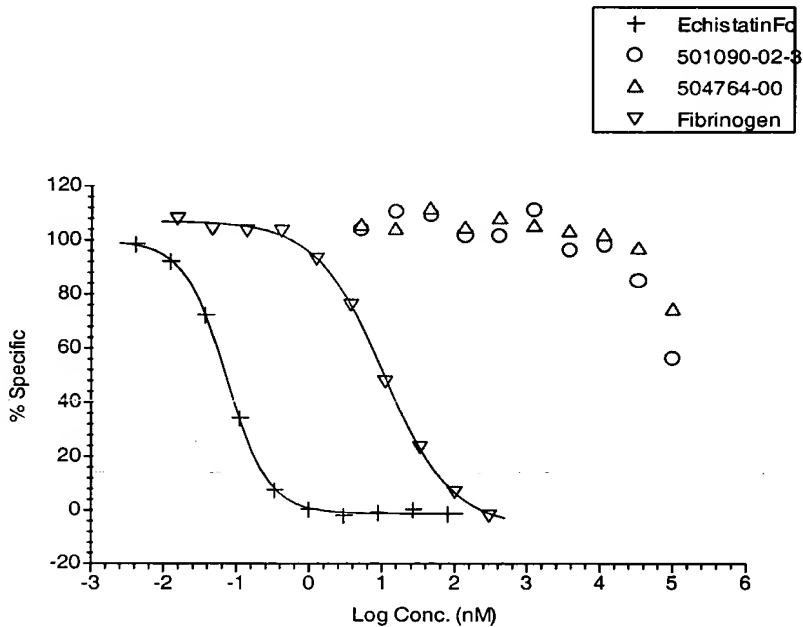
Inhibition of hu Vitronectin-Ru Binding to $\alpha v \beta 3$



Conc.		IC50 IP	Hill Slope	r2	Ki
AMG	504823-05	26.73786	-1.14	1.000	21.10884
Conc.		IC50 IP	Hill Slope	r2	Ki
AMG	EchistatinFc	0.12722	-1.10	0.999	0.10044
Conc.		IC50 IP	Hill Slope	r2	Ki
AMG	504849-02	>10000			>10000
Conc.		IC50 IP	Hill Slope	r2	Ki
AMG	501090-02-3	22.33247	-1.04	0.997	17.63090

FIGS. 5A and 5B

Inhibition of hu Fibrinogen-Ru Binding To



nM

Conc.		IC50 IP	r2	Ki
AMG	EchistatinFc	0.07187	1.000	0.03594

Conc.		IC50 IP	r2	Ki
AMG	501090-02-3	>100000		>100000

Conc.		IC50 IP	r2	Ki
AMG	504764-00	>100000		>100000

Conc.		IC50 IP	r2	Ki
AMG	Fibrinogen	10.51409	0.999	5.25705